Please amend claims 1-10 as follows:

1. (Amended) A method of testing a subject to determine if the subject has a predisposition for developing breast cancer which comprises detecting a mutation in the open reading frame of the ATM gene (SEQ.ID.NO: 1) in a cDNA sample prepared from a mRNA sample or a genomic DNA sample from the subject; which mutation is selected from the group consisting of the mutations set forth in Table 4 and wherein the presence of such mutation indicates that the subject has a predisposition for developing breast cancer.

2. (Amended) The method according to claim 1, wherein said detecting step includes detecting DNA characterized by including at least one mutation selected from the group consisting of the following mutations: position 3161 C->G; position 2572 T->C; position 6235 G->A; position 3118 A->G; position 378 T->A; position 2614 C->T; position 146 C->G; and position 1636 C->G.

3. (Amended) The method according to claim 1, wherein said detecting step includes detecting DNA characterized by including at least two mutations selected from the group consisting of the following double mutations: positions 3161 C->G and 2572 T->C; and positions 6235 G->A and 378 T->A.

4. (Amended) A method of testing a subject, who has already developed primary breast cancer, to determine if the subject has a predisposition to develop bilateral breast cancer which comprises detecting a mutation in the open reading frame of the ATM gene (SEQ.ID.NO: 1) in a cDNA sample prepared from a mRNA sample, or in a genomic DNA sample, from the subject; which mutation is selected from the group consisting of the mutations set forth in Table 4 and and wherein the presence of such mutation indicates that the subject has a predisposition to develop bilateral breast cancer.

5. (Amended) The method according to claim 4, wherein said detecting step includes detecting DNA characterized by including at least one mutation selected from the group consisting of the following mutations: position 3161 C->G; position 2572 T->C; position 6235 G->A; position 3118 A->G; position 378 T->A; position 2614 C->T; position 146 C->G; and position 1636 C->G.

6. (Amended) The method according to claim 4, wherein said detecting step includes detecting DNA characterized by including at least two mutations selected from the group consisting of the following double mutations: positions 3161 C->G and 2572 T->C; and positions 6235 G->A and 378 T->A.

7. (Amended) An isolated cDNA comprising consecutive nucleotides having a nucleotide sequence which differs from the sequence set forth in SEQ ID NO. 1 by a mutation selected from the group consisting of the following mutations: position 378 T->A; position 3383 A->G; position 1636 C->G; position 2614 C->T; position 6437 G->C; position 2932 T->C; position 2289 T->A; position 6096 A->T; position 6176 C->T; position 6919 C->T; position 2442 C->A; position 3925 G->A; position 6067 G->A; position 2119 T->C; position 1810 C->T; and position 4388 T->G.

8. (Amended) A marker for determining a predisposition for breast cancer, wherein said marker includes a mutation in the open reading frame of the ATM gene (SEQ ID NO: 1), which mutation results in a change in the amino acid sequence encoded thereby.

9. (Amended) The marker according to claim 8, wherein said mutation is selected from the group consisting of the mutations set forth in Table 4.

10. (Amended) The marker according to claim 9, wherein said mutation is selected from the group consisting of the following mutations: position 378 T->A; position 3383 A->G; position 1636 C->G; position 2614 C->T; position 6437 G->C;

position 2932 T->C; position 2289 T->A; position 6096 A->T; position 6176 C->T; position 6919 C->T; position 3925 G->A; position 6067 G->A; position 2119 T->C; position 1810 C->T; and position 4388 T->G.

Please add claims 11-22 as follows:

--11. (New) The method according to claim 1, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 2119 T->C.--

--12. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 3161 C->G.--

--13. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 2572 T->C.--

--14. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 6235 G->A.--

--15. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 3118 A->G.--

--16. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 378 T->A.--

--17. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 2614 C->T.--

--18. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 146 C->G.--

--19. (New) The method according to claim 2, wherein said detecting step includes detecting DNA characterized by including the following mutation: position 1636 C->G.--

--20. (New) The method according to claim 1, wherein said detecting step includes detecting DNA characterized by including at least two mutations from Table 4, one of which is 2119 T->C.--

--21. (New) The method according to claim 3, wherein the double mutation is positions 3161 C->G and 2572 T->C.--

--22. The method according to claim 3, wherein the double mutation is positions 6235 G->A and 378 T->A.--

A marked-up version of the amendments made herein is attached hereto as **Exhibit A**. Support for the preceding amendments to certain claims and for new claims can be found throughout the specification as filed. Specifically, amendments to claims 1-9 were made to delete reference to Table 5 and to simplify claim language. The amendment to claim 10 was made to correct a minor clerical error. Support for new claims 11-20 can be found, inter alia, in Table 4 on pages 19-20. Support for claims 21 and 22 can be found, inter alia, on page 23, 1st paragraph. Moreover, each of the new claims 11-22 merely reflect a subset of subject matter of the claims from which they depend.

REMARKS

Claims 1-10 were pending in the subject application. Applicants hereinabove have amended claims 1-10 and added new claims 11-22. Accordingly, claims 1-22 are now pending and presented for the Examiner's consideration.

Restriction Requirement

In the August 30, 2002 Office Action, the Examiner required restriction to a single nucleic acid sequence, The Office Action further requires restriction of the claims which require two or more mutations to a single mutation or combination of mutations.

The Examiner alleged that each marker/sequence is patentably distinct because they are unrelated sequences. The Examiner further alleges that these sequences are unrelated because the